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Education:

Conservatoire National des Arts et Métiers, 2008-present
PhD Candidate in Bioinformatics

Johns Hopkins University, 2003-2005
MHS in Biostatistics

Utah State University, 1996-2003
BS in Statistics
BS in Computational Mathematics
Minor in Computer Science

Professional Experience:

Basic Research Program, SAIC-Frederick, Inc. at NCI Frederick,
Bioinformatics Group, BSP CCR Genetics Core: June 2010 - Present
Bioinformatics Analyst: Provide statistical and technical support to NCI
labs within the Center for Cancer Research. Main projects supported
include genome-wide association studies, whole exome sequencing
studies, population admixture studies, and development of bioinformatics
tools.

Basic Research Program, SAIC-Frederick, Inc. at NCI Frederick,
Bioinformatics Section, Laboratory of Genomic Diversity: Feb 2004 - June 2010
Bioinformatics Analyst: Collaborate on grant proposals, manuscripts, and
development of new statistical tools. Provide statistical and technical
support to the lab. Teach seminars and short courses on statistical
methodology. Review and implement new statistical methods. Administer
local servers.

Johns Hopkins University: Aug 2004 – Dec 2004
Teaching Assistant: Grade homework and tests for Statistical Reasoning
course.

Utah State University: Aug 2002 – May 2003

Teaching Assistant: Taught fundamental methods of statistical data analysis in a business statistics recitation, and data management and mathematical modeling of populations in two ecology laboratory sections.

Tutor: Tutored small groups and individuals in statistics.

Human Genetics Section, Laboratory of Genomic Diversity at NCI-Frederick:
Jun 2002 – Aug 2002

Cancer Research Training Assistantship: Statistical analysis of HLA genetics in individuals with AIDS and various cancers.

Utah State University, Center for Persons with Disabilities, Biomedical Lab:
Jun 2001 – May 2002

Data Analyst: Statistical analysis of HLA genetics in families with autistic children.

Technical Skills:

R scripting and statistical analysis

R package development

Data/database management

Word processing, including LaTeX and Word

Mac OS X, Windows, UNIX/Linux

Familiarity with other programming languages including SAS, C, SQL, & Perl

Organization Memberships:

American Statistical Association

American Society of Human Genetics

National Eagle Scout Association

Publications:

Johnson RC, Nelson GW, Troyer JL, Lautenberger JA, Kessing BD, Winkler CA, O'Brien. **Accounting for multiple comparisons in a genome-wide association study (GWAS)**, *BMC Genomics*, 2010, (*In press*)

Nelson GW, Freedman BI, Bowden DW, Langefeld CD, An P, Hicks PJ, Bostrom MA, **Johnson RC**, Kopp JB, Winkler CA. **Dense mapping of MYH9 localizes the strongest kidney disease associations to the region of introns 13 to 15**, *Human Molecular Genetics*, 2010, 19 (9), 1805-15

O'Connor SL, Lhost JJ, Becker EA, Detmer AM, **Johnson RC**, Macnair CE, Wiseman RW, Karl JA, Greene JM, Burwitz BJ, Bimber BN, Lank SM, Tuscher JJ, Mee ET, Rose NJ, Desrosiers RC, Hughes AL, Friedrich TC, Carrington M, O'Connor DH. **MHC heterozygote advantage in simian immunodeficiency virus-infected Mauritian cynomolgus macaques**, *Science Translational Medicine*, 2010, 2 (22), 22ra18

An P, **Johnson RC**, Phair J, Kirk GD, Yu XF, Donfield S, Buchbinder S, Goedert JJ, Winkler CA. **Loss of *APOBEC3B* Gene Increases Risk of HIV-1 Acquisition**, *Journal of Infectious Diseases*, 2009, 200 (7), 1054-8

Roelke ME, Brown MA, Troyer JL, Winterbach H, Winterbach C, Hemson G, Smith D, **Johnson RC**, Pecon-Slaterry J, Roca AL, Alexander K, Klein L, Martinelli P, Krishnasamu K, O'Brien SJ. **Pathological Manifestations of Feline Immunodeficiency Virus (FIV) Infection in Wild African Lions**, *Virology*, 2009, 390 (1), 1-12

Streeck H, Jolin JS, Qi Y, Yassine-Diab B, **Johnson RC**, Kwon DS, Addo MM, Brumme C, Routy JP, Little S, Jessen HK, Kelleher AD, Hecht FM, Sekaly RP, Rosenberg ES, Walker BD, Carrington M, Altfeld M. **HIV-1-Specific CD8+ T Cell Responses During Primary Infection are Major Determinants of the Viral Set Point and Loss of CD4+ T Cells**, *Journal of Virology*, 2009, 83 (15), 7641-8

Winkler CA An P, **Johnson RC**, Nelson GW, Kirk G. **Expression of Duffy Antigen Receptor for Chemokines (DARC) has no Effect on HIV-1 Acquisition or Progression to AIDS in African Americans**, *Cell Host & Microbe*, 2009, 5 (5), 411-13

Guo X, **Johnson RC**, Deng H, Liao J, Guan L, Nelson GW, Tang M, Zheng Y, de The G, O'Brien SJ, Winkler CA, Zeng Y. **Evaluation of Nonviral Risk Factors for Nasopharyngeal Carcinoma in a High-Risk Population of Southern China**, *International Journal of Cancer*, 2009, 124 (12), 2942-7

Kopp JB, Smith MW, Nelson G, **Johnson RC**, Freedman BI, Bowden DW, Oleksyk T, McKenzie LM, Kajiyama H, Ahuja TS, Berns JS, Briggs W, Cho ME, Dart RA, Kimmel PL, Korbet SM, Michel DM, Mokrzycki MH, Schelling JR, Simon E, Trachtman H, Vlahov D, Winkler CA. ***MYH9* is a Major-Effect Risk Gene for Focal Segmental Glomerulosclerosis**, *Nature Genetics*, 2008, 40 (10), 1175-84

Hendrickson SL, Jacobson LP, Nelson GW, Phair JP, Lautenberger J, **Johnson RC**, Kingsley L, Margolick JB, Detels R, Goedert JJ, O'Brien SJ. **Host Genetic Influences on HAART Efficacy and AIDS-Free Survival**, *Journal of Acquired Immune Deficiency Syndromes*, 2008, 48 (3), 263-71

Hutcheson HB, Lautenberger JA, Nelson GW, Pontius JU, Kessing BD, Winkler CA, Smith MW, **Johnson RC**, Stephens R, Phair J, Goedert JJ, Donfield S, O'Brien SJ. **Detecting AIDS restriction genes: From candidate genes to genome-wide association discovery**, *Vaccine*, 2008, 26 (24), 2951-65

Bashirova AA, Bleiber G, Qi Y, Hutcheson H, Yamashita T, **Johnson RC**, Cheng J, Alter G, Goedert J, Buchbinder S, Hoots K, Vlahov D, May M, Maldarelli F, Jacobson L, O'Brien SJ, Telenti A, Carrington M. **Consistent Effects of TSG101 Genetic Variability on Multiple Outcomes of Exposure to Human Immunodeficiency Virus Type 1**, *Journal of Virology*, 2006, 80 (14), 6757-63

Guo XC, Scott K, Liu Y, Dean M, David V, Nelson GW, **Johnson RC**, Dilks HH, Lautenberger J, Kessing B, Martenson J, Guan L, Sun S, Deng H, Zheng Y, de The G, Liao J, Zeng Y, O'Brien SJ, Winkler CA. **Genetic factors leading to chronic Epstein-Barr virus infection and nasopharyngeal carcinoma in South East China: Study design, methods and feasibility**, *Human Genomics*, 2006, 2 (6), 365-75

Yant LJ, Friedrich TC, **Johnson RC**, May G, Maness NJ, Enz AM, Lifson JD, O'Connor DH, Carrington M, Watkins DI. **The High Frequency MHC Class I Allele *Mamu-B*17* is Associated with Control of SIVmac239 Replication**, *Journal of Virology*, 2006, 80 (10), 5074-7

Software:

Warnes GR, Includes R source code and/or documentation contributed by Bolker B, Lumley T, **Johnson RC**. **gmodels: Various R programming tools for model fitting**, <http://www.sf.net/projects/r-gregmisc>

Maindonald JH, with hwexact() from **Johnson RC**. **hwde: Models and tests for departure from Hardy-Weinberg equilibrium and independence between loci**, <http://www.maths.anu.edu.au/~jhonm>

Patent:

Winkler CA, Kopp JB, Smith MW, Nelson GW, **Johnson RC**. **Single Nucleotide Polymorphism Associated with Renal Disease**, *PTC Patent Application*, (PCT/US2009/032754)